

FIG. 1

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LINKER #1 15bp | SV40 ORIGIN=332bp
GACGTCGGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCA 60
AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
GGAGAAATGGG CGGAACCTGGG CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT 180
ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCACTTC TGCTGCTGG GGAGCCTGGG 240
GACTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
GGGGAGCCTG GGGACTTCC ACACCCCTAAC TGACACACAT TCCACAGAAAT TAATTCCCC 360
347 8 360 1
AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATCA GCCCATATAT GGAGTTCCGC 420
GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480
CMV PROMOTER-ENHANCER=567bp
ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTCCCA TTGACGTCAA 540
TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTAT CATATGCCA 600
AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATT TGCCAGTAC 660
ATGACCTTAT GGGACTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
ATGGTGATGC GGTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTGA CTCACGGGGA 780
TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTGT TTTGGCACCA AAATCAACGG 840
GACTTCCAA AATGTCGTA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTAA 900
LINKER #3=76bp
CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
727 8
Bgl II LEADER=60bp
CATCACAGAT CTCTCACCAT GAGGGTCCCC GCTCAGCTCC TGGGGCTCCT GCTGCTCTGG 1020
978 9
+1 101 102 107 108
CTCCCAGGTG CACGATGTGA TGGTACCAAG GTGGAAATCA AACGTACGGT GGCTGCACCA 1080
1038 9 1062 3 Bsi WI
TCTGTCTTCA TCTTCCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACCTGC CTCTGTTGTG 1140
TGCCTGCTGA ATAACCTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAAGGT GGATAACGCC 1200
HUMAN KAPPA CONSTANT 324bp 107 AMINO ACID & STOP CODON
CTCCAATCGG GTAACCTCCA GGAGAGTGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1260
AGCCTCAGCA GCACCCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1320
TGCAGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTACCAA AGAGCTTCAA CAGGGGAGAG 1380
STOP
LIGHT
CHAIN Eco RI LINKER #4=85bp
TGTTCGAATTG AGATCCGTAA ACGGTTACCA ACTACCTAGA CTGGATTGCGT GACAACATGC 1440
1386 7
GGCGGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500
1471 2

FIG. 2A

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GTTTGCCTT CCCCCGTGCC TTCCCTGACC CTGGAAAGGTG CCACCTCCCAC TGTCCCTTCC 1560
BGH poly A=231bp
TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620
GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680
LINKER #5=15bp
GCGGTGGGCT CTATGGAACC AGCTGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740
1702₃ 1717₈
ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCA GTACATGACC TTATGGACT 1800
TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTT 1860
CMV PROMOTER-ENHANCER=334bp
GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTCCA AGTCTCCACC 1920
CCATTGACGT CAATGGGAGT TTGTTTGGC ACCAAAATCA ACAGGGACTTT CCAAAATGTC 1980
GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
LINKER #6=7bp
TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2100
2051₂ 2058₉ Sal I
ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACGGCTGT CGCTAGCACC 2160
START HEAVY CHAIN -5 -4 -3 114 115
LEADER=51bp Mlu I 2151₂ Nhe I
AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACACCG 2220
GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 2280
GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 2340
HUMAN GAMMA 1 CONSTANT
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 2400
993bp=330 AMINO ACID & STOP CODON
AACGTGAATC ACAAGCCCCAG CAACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT 2460
GACAAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 2520
TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCGGACCCCC TGAGGTCACA 2580
TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640
GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 2700
CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGACTACAAG 2760
TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820
GGGCAGCCCC GAGAACCAAC GGTGTACACC CTGCCCCAT CCGGGATGA GCTGACCAGG 2880
AACCCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 2940
TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 3000

FIG. 2B

GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 3060
 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120
 STOP HEAVY CHAIN Bam HI LINKER #7=81bp
 CTCTCCCTGT CTCCGGGTAA ATGAGGATCC GTTAACGGTT ACCAACTACC TAGACTGGAT 3180
 3144₁₅
 TCGTGACAAC ATGCGGCCGT GATATCTACG TATGATCAGC CTCGACTGTG CCTTCTAGTT 3240
 3225₁₆
 GCCAGCCATC TGTTGTTGC CCCTCCCCG TGCTTCTT GACCCCTGGAA GGTGCCACTC 3300
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 CCACTGTCCT TTCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT 3360
 CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGA GGATTGGGAA GACAATACCA 3420
 LINKER #8=34bp
 GGCATGCTGG GGATGCGGTG GGCTCTATGG AACCAGCTGG GGCTCGACAG CGCTGGATCT 3480
 3456₁₇
 CCCGATCCCC AGCTTGCTT CTCATAATTCT TATTCGATA ATGAGAAAAA AAGGAAAATT 3540
 3490₁
 AATTTAACCA CAAATTCACT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 3600
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 3660
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 3720
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 3780
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTGCTT 3840
 LINKER #9=19bp 5' UNTRANSLATED DHFR=82bp
 CTGACATAGT TGTGTTGGGA GCTTGGATAG CTTGGACAGC TCAGGGCTGC GATTCGCGC 3900
 3856₁₇ 3875₁₆ START DHFR
 CAAACTTGAC GGCAATCCTA GCGTGAAGGC TGTTAGGATT TTATCCCCGC TGCCATCATA 3960
 3957₁₈
 GTTCGACCAT TGAACTGCAT CGTCGCCGTG TCCCAAAATA TGGGGATTGG CAAGAACGGA 4020
 GACCTACCCCT GGCTCCGCT CAGGAACGAG TTCAAGTACT TCCAAAGAAT GACCACAACC 4080
 TCTTCAGTGG AAGGTAAACA GAATCTGGTG ATTATGGTA GGGAAACCTG GTTCTCCATT 4140
 MOUSE DHFR=564bp=187 AMINO ACID & STOP CODON
 CCTGAGAAGA ATCGACCTTT AAAGGACAGA ATTAATATAG TTCTCAGTAG AGAACTCAAA 4200
 GAACCACCAAC GAGGAGCTCA TTTCTTGCC AAAAGTTGG ATGATGCCTT AAGACTTATT 4260
 GAACAAACCGG AATTGGCAAG TAAAGTAGAC ATGGTTGGA TAGTCGGAGG CAGTTCTGTT 4320
 TACCAAGGAAG CCATGAATCA ACCAGGCCAC CTTAGACTCT TTGTGACAAG GATCATGCAG 4380
 GAATTGAAA GTGACACGTT TTTCCCAGAA ATTGATTGG GGAAATATAA ACTTCTCCCA 4440
 GAATAACCCAG GCGTCCTCTC TGAGGTCCAG GAGGAAAAAG GCATCAAGTA TAAGTTGAA 4500

FIG. 2C

STOP DHFR
 GTCTACGAGA AGAAAGAC ~~TA~~ ACAGGAAGAT GCTTCAAGT TCTCTGCTCC CCTCCTAAAG 4560
 4521 2

3' UNTRANSLATED DHFR=82bp LINKER #10=10bp
 TCATGCATTT TTATAAGACC ATGGGACTTT TGCTGGCTTT AGATCAGCCT CGACTGTGCC 4620
 4603 4 4613 4

TTCTAGTTGC CAGCCATCTG TTGTTTGCCC CTCCCCCGTG CCTTCCTTGA CCCTGGAAAGG 4680
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 TGCCACTCCC ACTGTCTTT CCTAATAAAA TGAGGAAATT GCATCGCATT GTCTGAGTAG 4740

GTGTCAATTCT ATTCTGGGGG GTGGGGTGGG GCAGGACAGC AAGGGGGAGG ATTGGGAAGA 4800
 CAATAGCAGG CATGCTGGGG ATGCCGGTGGG CTCTATGGAA ~~CCAGCTGGGG~~ CTCGAGCTAC 4860
 4844 5

TAGCTTGCT TCTCAATTTC TTATTTGCAT AATGAGAAAA AAAGGAAAAT TAATTTAAC 4920

ACCAATTCAAG TAGTTGATTG AGCAAATGCG TTGCCAAAAA GGATGCTTA GAGACAGTGT 4980
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 TCTCTGCACA GATAAGGACA AACATTATTC AGAGGGAGTA CCCAGAGCTG AGACTCCTAA 5040

GCCAGTGAGT GGCACAGCAT TCTAGGGAGA AATATGCTTG TCATCACCGA AGCCTGATT 5100

CGTAGAGCCA CACCTTGGTA AGGGCCAATC TGCTCACACA GGATAGAGAG GGCAGGAGCC 5160

AGGGCAGAGC ATATAAGGTG AGGTAGGATC AGTTGCTCCT CACATTGCT TCTGACATAG 5220

LINKER #12=21bp START NEO
 TTGTGTTGGG AGCTTGGATC GATCCTCTAT ~~GTTGAACAA~~ GATGGATTGC ACGCAGGTT 5280
 5227 8 5248 9

TCCGGCCGCT TGGGTGGAGA GGCTATTGG CTATGACTGG GCACAACAGA CAATGGCTG 5340

CTCTGATGCC GCCGTGTTCC GGCTGTCAGC GCAGGGGCCGC CCGGTTCTTT TTGTCAAGAC 5400

NEOMYCIN PHOSPHOTRANSFERASE
 CGACCTGTCC GGTGCCCTGA ATGAACTGCA GGACGAGGCA GCGGGCTAT CGTGGCTGGC 5460

795bp=264 AMINO ACIDS & STOP CODON
 CACGACGGGC GTTCCTGCG CAGCTGTGCT CGACGTTGTC ACTGAAGCGG GAAGGGACTG 5520

GCTGCTATTG GGCGAAGTGC CGGGGCAGGA TCTCCTGTCA TCTCACCTTG CTCCCTGCCGA 5580

GAAAGTATCC ATCATGGCTG ATGCAATGCG GCGGCTGCAT ACGCTTGATC CGGCTACCTG 5640

CCCATTGAC CACCAAGCGA AACATCGCAT CGAGCGAGCA CGTACTCGGA TGGAAAGCCGG 5700

TCTTGTGAT CAGGATGATC TGGACGAAGA GCATCAGGGG CTCGGGCCAG CCGAACTGTT 5760

CGCCAGGCTC AAGGGCGCCGA TGCCCCACGG CGAGGATCTC GTCGTGACCC ATGGCGATGC 5820

CTGCTTGGCG AATATCATGG TGGAAAATGG CCGCTTTCT GGATTCACTG ACTGTGGCCG 5880

GCTGGGTGTG GCGGACCGCT ATCAGGACAT AGCGTTGGCT ACCCGTGATA TTGCTGAAGA 5940

GCTTGGCGGC GAATGGGCTG ACCGCTTCCT CGTGCTTTAC GGTATCGCCG CT~~T~~CCCGATT 6000

FIG. 2D

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STOP NEO
GCAGCGCATC GCCTTCTATC GCCTTCTTGA CGAGTTCTTC TGAGCGGGAC TCTGGGGTTC 6060
6043¹⁴
GAAATGACCG ACCAAGCGAC GCCCAACCTG CCATCACGAG ATTCGATT CACCGCCGCC 6120
3' UNTRANSLATED NEO=173bp
TTCTATGAAA GGTTGGGCTT CGGAATCGTT TTCCGGGACG CCGGCTGGAT GATCCTCCAG 6180
CGCGGGGATC TCATGCTGGA GTTCTTCGCC CACCCCCAACT TGTTTATTGC AGCTTATAAT 6240
6216⁷
GGTTACAAAT AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTT TTCACTGCAT 6300
SV40 POLY A EARLY=133bp LINKER #13=19bp
TCTAGTTGTG GTTTGTCCAA ACTCATCAAT CTATCTTATC ATGTCGGAT CGCGGCCCG 6360
6349⁵⁰
ATCCCGTCGA GAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC 6420
6368⁹
CGCTCACAAAT TCCACACAAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT 6480
AATGAGTGAG CTAACTCACA TTAATTGCGT TGCGCTCACT GCCCGCTTTC CAGTCGGAA 6540
ACCTGTCGTG CCAGCTGCAT TAATGAATCG GCCAACCGCGC GGGGAGAGGGC GGTTTGCCTA 6600
PVC 19
TTGGGCGCTC TTCCGCTTCC TCGCTCACTG ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC 6660
GAGCGGTATC AGCTCACTCA AAGGCGGTAA TACGGTTATC CACAGAATCA GGGGATAACG 6720
CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCCGGT 6780
6792=BACTERIAL ORIGIN OF REPLICATION
TGCTGGCGTT TCTCCATAGG CTCCGCCCG CTGACGAGCA TCACAAAAAT CGACGCTCAA 6840
GTCAGAGGTG GCGAAACCCG ACAGGACTAT AAAGATACCA GGCCTTCCC CCTGGAAGCT 6900
CCCTCGTGCCT CTCTCCTGTT CCGACCCCTGC CGCTTACCGG ATACCTGTCC GCCTTCTCC 6960
CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG 7020
TCGTTCGCTC CAAGCTGGC TGTCGCACG AACCCCCCGT TCAGCCCCGAC CGCTGCGCCT 7080
TATCCGGTAA CTATCGTCTT GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG 7140
CAGCCACTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA 7200
AGTGGTGGCC TAACTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA 7260
AGCCAGTTAC CTTCGGAAAA AGAGTTGGTA GCTCTTGCATC CGGCAAACAA ACCACCGCTG 7320
GTAGCGGTGG TTTTTTGTT TGCAAGCAGC AGATTACCGCG CAGAAAAAAA GGATCTCAAG 7380
AAGATCCTTT GATCTTTCT ACGGGGTCTG ACGCTCAGTG GAACGAAAAC TCACGTTAAG 7440
GGATTTGGT CATGAGATTA TCAAAAAGGA TCTTCACCTA GATCCTTTA AATTAAAAAT 7500

FIG. 2E

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STOP BETA LACTAMASE
GAAGTTTAA ATCAATCTAA AGTATATATG AGTAAACCTTG GTCTGACAGT TACCAATGCT 7560
7550
TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTCG TTCATCCATA GTTGCCTGAC 7620
TCCCCGTCGT GTAGATAACT ACGATAACGGG AGGGCTTACC ATCTGGCCCC AGTGCTGCAA 7680
TGATACCGCG AGACCCACGC TCACCGGCTC CAGATTATC AGCAATAAAC CAGCCAGCCG 7740
GAAGGGCCGA GCGCAGAAGT GGTCTGCAA CTTTATCCGC CTCCATCCAG TCTATTAATT 7800
BETA LACTAMASE=861bp
286 AMINO ACID & STOP CODON
GTTGCCGGGA AGCTAGAGTA AGTAGTTCGC CAGTTATAG TTTGCGCAAC GTTGTGCCA 7860
TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT GGCTTCATTC AGCTCCGGTT 7920
CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAAGCG GTTAGCTCCT 7980
TCGGTCCTCC GATCGTTGTC AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG 8040
CAGCACTGCA TAATTCTCTT ACTGTCATGC CATCCGTAAG ATGCTTTCT GTGACTGGTG 8100
AGTACTCAAC CAAGTCATTC TGAGAATAGT GTATGCGGCG ACCGAGTTGC TCTTGCCCGG 8160
CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA 8220
AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTTCGATGT 8280
AACCCACTCG TGCAACCAAC TGATCTTCAG CATCTTTAC TTTCACCAAGC GTTTCTGGGT 8340
GAGCAAAAAC AGGAAGGCCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT 8400
START BETA LACTAMASE
GAATACTCAT ACTCTTCCTT TTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
8410
TGAGCGGATA CATATTTGAA TGTATTTAGA AAAATAAACAA AATAGGGGTT CCGCGCACAT 8520
TTCCCCGAAA AGTGCCACCT

FIG. 2F

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LINKER #1=15bp
GACGTCGGCGG CCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
15 6

AGGCCGAGGC GGCCCTGGCC TCTGCATAAAA TAAAAAAAAT TAGTCAGCCA TGCA~~TGGGC~~ 120

SV40 ORIGIN=332bp
GGAGAA~~TGGG~~ CGGA~~ACTGGG~~ CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT 180

ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240

GA~~CTTCCAC~~ ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300

GGGGAGCCTG GGGACTTCC ACACC~~TAAC~~ TGACACACAT TCCACAGAA~~T~~ TAATTCCCCT 360
347 8

AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCAT~~A~~ GCCCATATAT GGAGTTCCGC 420

GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480

ACGTCAATAA TGACGTATGT TCCC~~CATAGTA~~ ACGCCAA~~TAG~~ GGACTTTCCA TTGACGTCAA 540

CVM PROMOTER-ENHANCER=567bp
TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600

AGTACGCC~~CC~~ CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATT~~A~~ TGCCCAGTAC 660

ATGACCTTAT GGGACTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720

ATGGTGATGC GGTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTGA CTCACGGGG 780

TTTCCAAGTC TCCACCCCCAT TGACGTCAAT GGGAGTTGT TTTGGCACCA AAATCAACGG 840

GA~~CTTCCAA~~ AATGT~~CGTAA~~ CAACTCCGCC CCATTGACGC AAATGGGC~~GG~~ TAGGC~~GTG~~TA 900

CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACG~~T~~GAACC GTCAGATCGC CTGGAGACGC 960
927 8 934 5

Bgl 2 START LIGHT CHAIN NATURAL LEADER=66bp
CATCACAGAT CTCTCACTAT GGATTTCA~~G~~ GTGCAGATT~~A~~ TCAGCTT~~C~~ GCTAATCAGT 1020
978 9

GCTTCAGTCA TAATGTCCAG AGGACAA~~ATT~~ GTTCTCTCCC AGTCTCCAGC AATCCTGTCT 1080
1044 5+1

GCATCTCCAG GGGAGAAGGT CACAATGACT TGCA~~GGGCCA~~ GCTGAAGTGT AAGTTACATC 1140

CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCC~~T~~ GGATTTATGC CACATCCAAC 1200

LIGHT CHAIN VARIABLE REGION 318bp 106 AMINO ACID
CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCA~~G~~TGGGT CTGGGACTTC TTACTCTCTC 1260

ACCATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT 1320

AACCCACCCA CGTTGGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCACCA 1380
1362 3

TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACTGC CTCTGTTGTG 1440

TGCCTGCTGA ATAAC~~T~~CTA TCCCAGAGAG GCCAAAGTAC AGTGGAGGT GGATAACGCC 1500

FIG. 3A

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HUMAN KAPPA CONSTANT=324bp=107 AMINO ACID & STOP CODON
CTCCAATCGG GTAACTCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1560
AGCCTCAGCA GCACCCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1620
TGCAGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTACCAA AGAGCTTCAA CAGGGGAGAG 1680
STOP
LIGHT
CHAIN Eco RI LINKER #4=81bp
TGTGAATT AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTGCGT GACAACATGC 1740
1646 7
GGCGTGTATA TCTACGTATG ATCAGCCTCG ACTGTGCCCT TAGTTGCCA GCCATCTGTT 1800
1771 2
GTTTGCCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAAGGTG CCACCTCCCAC TGCCCTTCC 1860
TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1920
BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1980
LINKER #5=15bp
GCGGTGGGCT CTATGGAACC AGCTGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 2040
2002 3 2017 8
ACGTCAATGA CGGTAAATGG CCCCCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 2100
TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 2160
CMV PROMOTER-ENHANCER=334bp
GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC 2220
CCATTGACGT CAATGGGAGT TTGTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 2280
GTAACAAACTC CGCCCCATTG ACGAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2340
LINKER #6=7bp Sal I
TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2400
START 2351 2 2358 9
HEAVY CHAIN SYNTHETIC & NATURAL LEADER Mlu I 2457 8
ATGGGTTGGA GCCTCATCTT GCTCTTCCCTT GTCGCTGTTG CTACGGCTGT CCTGTCCCCAG 2460
2401 -5 -4 -3 -2 -1 +1
GTACAACTGC AGCAGCCTGG GGCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATGTCC 2520
TGCAAGGCTT CTGGCTACAC ATTACCACT TACAATATGC ACTGGGTAAA ACAGACACCT 2580
HEAVY CHAIN VARIABLE=363bp=121 AMINO ACID
GGTCGGGGCC TGGAAATGGAT TGGAGCTATT TATCCCGGAA ATGGTGATAAC TTCTACAAT 2640
CAGAAGTTCA AAGGCAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 2700
CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ACTGTGCAAG ATCGACTTAC 2760
TACGGCGGTG ACTGGTACTT CAATGTCTGG GGCGCAGGGA CCACGGTCAC CGTCTCTGCA 2820
Nhe I
GCTAGCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG 2880
GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTG 2940
HUMAN GAMMA 1 CONSTANT=993bp
TGGAACTCAG GCGCCCTGAC CAGCGGCCTG CACACCTTCC CGGCTGTCT ACAGTCCTCA 3000

FIG. 3B

330 AMINO ACID & STOP CODON

GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 3060
 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGCAGAGCCC 3120
 AAATCTTGTG ACAAAAATCA CACATGCCA CCGTGCCCCAG CACCTGAACt CCTGGGGGGA 3180
 CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT 3240
 GAGGTACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG 3300
 TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC 3360
 AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCGCACC AGGACTGGCT GAATGGCAAG 3420
 GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC 3480
 AAAGCCAAAG GGCAGCCCCG AGAACCCACAG GTGTACACCC TGCCCCCATC CCGGGATGAG 3540
 CTGACCAAGA ACCAGGTCAg CCTGACCTGC CTGGTCAAAG GCTTCTATCC CAGCGACATC 3600
 GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAACT ACAAGACCAC GCCTCCCGTG 3660
 CTGGACTCCG ACGGCTCCTT CTTCCCTCTAC AGCAAGCTCA CCGTGGACAA GAGCAGGTGG 3720
 CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG 3780
 STOP HEAVY CHAIN (Bam HI) LINKER #7=81bp
 CAGAAGAGCC TCTCCCTGTC TCCGGTAAA TGAGGGATCCG TTAACGGTTA CCAACTACCT 3840
 3813 4
 AGACTGGATT CGTGACAAACA TGCGGCCGTG ATATCTACGT ATGATCAGCC TCGACTGTG 3900
 3894 5
 CTTCTAGTTG CCAGCCATCT GTTGTGTTGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAAE 3960
 GTGCCACTCC CACTGTCCCT TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA 4020
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 GGTGTCATTC TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGGAAG 4080
 ACAATAGCAG GCATGCTGGG GATGCGGTGG GCTCTATGGA ACCAGCTGGG GCTCGACAGC 4140
 4125 6
 GCTGGATCTC CCGATCCCCA GCTTTGCTTC TCAATTCTT ATTTGCATAA TGAGAAAAAA 4200
 AGGAAAATTA ATTTAACAC CAATTCAAGTA GTTGATTGAG CAAATGCGTT GCCAAAAAGG 4260
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 ATGCTTTAGA GACAGTGGTC TCTGCACAGA TAAGGACAAA CATTATTCAg AGGGAGTACC 4320
 CAGAGCTGAG ACTCCTAACG CAGTGAGTGG CACAGCATTc TAGGGAGAAA TATGCTTGTC 4380
 ATCACCGAAG CCTGATTCCG TAGAGCCACA CCTTGGTAAG GGCAATCTG CTCACACAGG 4440
 ATAGAGAGGG CAGGAGCCAG GGCAGAGCAT ATAAGGTGAG GTAGGGATCAg TTGCTCCTCA 4500

FIG. 3C

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CATTGCTTC TGACATAGTT LINKER #9=19bp 5' UNTRANSLATED DHFR=82bp
4525 6 4544 5
ATTCGCGCC AAACTTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATT TATCCCCGCT 4620
START DHFR
GCCATCATGG TTGACCATT GAACTGCATC GTGCGCGTGT CCCAAAATAT GGGGATTGGC 4680
4626 7
AAGAACGGAG ACCTACCCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740
ACCACAAACCT CTTCAGTGGA AGGTAAACAG AATCTGGTGA TTATGGTAG GAAAACCTGG 4800
DHFR=564bp=187 AMINO ACID & STOP CODON
TTCTCCATTG CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860
GAACCAAAG ACCAACCAACG AGGAGCTCAT TTTCTGCCA AAAGTTGGA TGATGCCTTA 4920
AGACTTATTG AACAAACCGGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980
AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040
ATCATGCAGG AATTGAAAG TGACACGTTT TTCCCAGAAA TTGATTTGGG GAAATATAAA 5100
CTTCTCCAG AATAACCCAGG CGTCCTCTCT GAGGTCCAGG AGGAAAAAAGG CATCAAGTAT 5160
STOP DHFR 3' UNTRANSLATED DHFR=82bp
AAGTTGAAG TCTACGAGAA GAAAGACTAA CAGGAAGATG CTTTCAAGTT CTCTGCTCCC 5220
5140 1
LINKER #10
CTCCTAAAGC TATGCATTT TATAAGACCA TGGGACTTTT GCTGGCTTTA GATCAGCCTC 5280
5272 3
=10bp
GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTGCCCCC TCCCCCGTGC CTTCCTTGAC 5340
BOVINE GROWTH HORMONE POLYADENYLATION=231bp
CCTGGAAAGGT GCCACTCCCCTGCTTCAATAAAAAT GAGGAAATTG CATCGCATGG 5400
TCTGAGTAGG TGTCAATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460
LINKER #11
TTGGGAAGAC AATAGCAGGC ATGCTGGGA TGCGGTGGC TCTATGGAAC CAGCTGGGGC 5520
5513 4
=17bp
TCGAGCTACT AGCTTGCTT CTCATTCT TATTGCTA ATGAGAAAAA AAGGAAAATT 5580
5530 1
AATTAAACA CCAATTCACT AGTTGATTGA GCAAATGCGT TGCCAAAAG GATGCTTAG 5640
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
AGACAGTGTT CTCTGCACAG ATAAGGACAA CTAGGGAGAA ATATGCTTGT CATCACCGAA 5700
GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 5760
GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820
GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTGCTT 5880
LINKER #12=21bp START NEO
CTGACATAGT TGTGTTGGGA GCTTGGATCG ATCCTCTATG GTTGAACAAG ATGGATTGCA 5940
5896 7 5917 8
CGCAGGTTCT CGGGCCGCTT GGGTGGAGAG GCTATTGGC TATGACTGGG CACAACAGAC 6000

FIG. 3D

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AATCGGCTGC TCTGATGCCG CCGTGTCCG GCTGTCAGCG CAGGGGCGTC CGGTTCTTT 6060
NEOMYCIN PHOSPHOTRANSFERASE=795bP=264 AMINO ACID & STOP CODON
TGTCAAGACC GACCTGTCCG GTGCCCTGAA TGAAC TGCAAGCAG CGCGGCTATC 6120
GTGGCTGGCC ACGACGGGGC TTCCCTGCCG AGCTGTGCTC GACGTTGTCA CTGAAGCGGG 6180
AAGGGACTGG CTGCTATTGG GCGAAGTGCC GGGGCAGGAT CTCCGTGATC CTCACCTTGC 6240
TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCCG CGGCTGCATA CGCTTGATCC 6300
GGCTACCTGC CCATTCGACC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360
GGAAGCCGGT CTTGTCGATC AGGATGATCT GGACGAAGAG CATCAGGGGC TCGCGCCAGC 6420
CGAACTGTTG GCCAGGCTCA AGGCGCGCAT GCCCGACGGC GAGGATCTCG TCGTGACCCA 6480
TGGCGATGCC TGCTTGCCGA ATATCATGGT GGAAAATGGC CGCTTTCTG GATTCATCGA 6540
CTGTGCCGG CTGGGTGTGG CGGACCGCTA TCAGGACATA GCCTTGGCTA CCCGTGATTAT 6600
TGCTGAAGAG CTTGGCGGGCG AATGGGCTGA CCGCTTCCTC GTGCTTTACG GTATCGCCGC 6660
STOP NEO
TCCCAGATTG CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTTCTG GAGCGGGACT 6720
6712³
CTGGGGTTCG AAATGACCGA CCAAGCGACG CCCAACCTGC CATCACGAGA TTTGATTCC 6780
3' UNTRANSLATED NEO=173bp
ACCGCCGCCT TCTATGAAAG GTTGGGCTTC GGAATCGTT TCCGGGACGC CGGCTGGATG 6840
ATCCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTCGCTC ACCCCAAACTT GTTTATTGCA 6900
6885⁶
GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATAA AGCATTTTT 6960
SV40 EARLY POLYADENYLATION REGION=133bp
TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATC TATCTTATCA TGTCTGGATC 7020
7018⁹
LINKER #13=19bp
GCGGCCGCGA TCCCCTCGAG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 7080
7037⁸
PUC 19
ATTGTTATCC GCTCACAAATT CCACACAAACA TAAGGAGCCGG AAGCATAAAG TGTAAGGCT 7140
GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTCC 7200
AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCG CCAACGCGCG GGGAGAGGCG 7260
GTTTGCCTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCCTC TCGGTGTT 7320
GGCTGCGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAAT ACGGTTAAC ACAGAATCAG 7380
GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAAG AACCGTAAAA 7440
7461=BACTERIAL ORIGIN OF REPLICATION
AGGCCGCGTT GCTGGCGTT TCCCATAGGC TCCGCCCGCC TGACGAGCAT CACAAAATC 7500

FIG. 3E

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GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAAG GCGTTTCCCC 7560
CTGGAAGCTC CCTCGTGCAGC TCTCCTGTT CGACCCCTGCC GCTTACCGGA TACCTGTCCG 7620
CCTTTCTCCC TTGGGGAAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT 7680
CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCCGTT CAGCCCGAC 7740
GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC 7800
CACTGGCAGC AGCCACTGGT AACAGGATTAA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860
AGTTCTTGAA GTGGTGGCCT AACTACGGCT ACACATAGAAG GACAGTATTG GGTATCTGCG 7920
CTCTGCTGAA GCCAGTTACC TTGGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA 7980
CCACCGCTGG TAGCGGTGGT TTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAAG 8040
GATCTCAAGA AGATCCTTTG ATCTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAAGT 8100
CACGTTAAGG GATTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTAA 8160
BETA LACTAMASE STOP 8220
ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTCGT TCATCCATAG 8280
TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA 8340
GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAAC 8400
BETA LACTAMASE=861bp=286 AMINO ACID & STOP CODON
AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCTGCAAC TTTATCCGCC TCCATCCAGT 8460
CTATTAATTG TTGCCGGAA GCTAGAGTAA GTAGTTGCC AGTTAATAGT TTGCGCAACG 8520
TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTGGTATG GCTTCATTCA 8580
GCTCCGGTTC CCAACGATCA AGGCAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8640
TTAGCTCCTT CGGTCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA 8700
TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTCTG 8760
TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT 8820
CTTGGCCGGC GTCAATAACCG GATAATAACCG CGCCACATAG CAGAACTTTA AAAGTGTCA 8880
TCATTGGAAA ACGTTCTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940
GGTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTACT TTCACCAAGCG 9000
TTTCTGGGTG AGCAAAAACA GGAAGGCAAATGCCGCAA AAAGGGAATA AGGGCGACAC 9060
GGAAATGTTG AATACTCAT START BETA LACTAMASE CTCTTCCTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120
ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC 9180
CGCCGACATT TCCCCGAAAAA GTGCCACCT

FIG. 3F

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LEADER

	-20		-15		-10			
FRAME 1	Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val							
	ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC							
	987	996	1005	1014	1023			
	Q	W	Q					
	-5	+1	+1	FR1		10		
Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser								
ATA ATG TCC AGA GGA ICAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT								
1038	1047	1056	1065	1074	1093			
	20	23	24	CDR1	27	29	30	34
Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Val Ser Tyr Ile His								
CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA AGT TAC ATC CAC								
1095	1104	1113	1122	1131	1140			
	35	FR2	40		45	49	50	CDR2
Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn								
TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT GCC ACA TCC AAC								
1152	1161	1170	1179	1188	1197			
	55	56	57	60	FR3	65	70	
Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser								
CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC AG GGG TCT GGG ACT TCT TAC TCT								
1209	1218	1227	1235	1245	1254			
	75		80		85	88	89	90
Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp								
CTC ACC ATC AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG								
1266	1275	1284	1293	1302	1311			
	CDR3	95	97	98	100	FR4	105	107
Thr Ser Asn Pro Pro Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys								
ACT AGT AAC CCA CCC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATC AAA								
1323	1332	1341	1350	1359				

FIG. 4

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LEADER

-19	-15	-10	-5
FRAME 1 Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val			
ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC			
2409	2418	2427	2436
2445			
-1	+1	10	15
Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys (Ala) Gly Ala Ser			
CTG TCC	CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG GCC TCA		
2460	2469	2478	2487
			2496 GCT
			2505
20	25	30	31 CDR1
Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp			
GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC AAT ATG CAC TGG			
2517	2526	2536	2544
			2553
			2562
40 FR2	45	49	50 52 52A 53 54
Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn			
GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA GCT ATT TAT CCC EGA AAT			
2574	2583	2592	2601
			2610
			2615
55 CDR2	60	65	66 FR3
Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys			
GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC AAG GCC ACA TTG ACT GCA GAC AAA			
2631	2640	2649	2658
			2667
			2676
75	80	82 82A 82B 82C 83	85
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val			
TCC TCC AGC ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC			
2688	2697	2706	2715
			2724
			2733
90	94 95	CDR3	100 100A 100B 100C 100D 101 102 103
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly			
TAT TAC TGT GCA AGA TCG ACT TAC TAC GGC GGT GAC TGG TAC TTC AAT GTC TGG GGC			
2745	2754	2763	2772
			2781
			2790
105 FR4	110	113	
Ala Gly Thr Thr Val Thr Val Ser Ala			
GCA GGG ACC ACG GTC ACC GTC TCT GCA			
2802	2811	2820	

FIG. 5

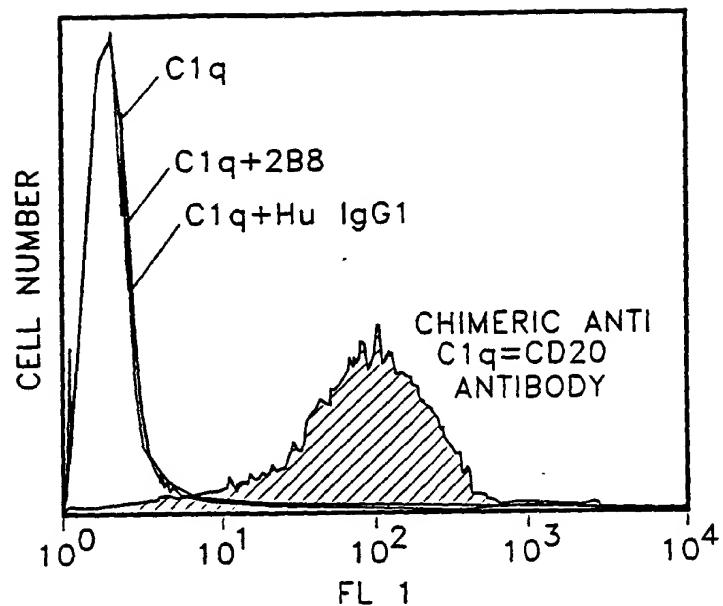


FIG. 6

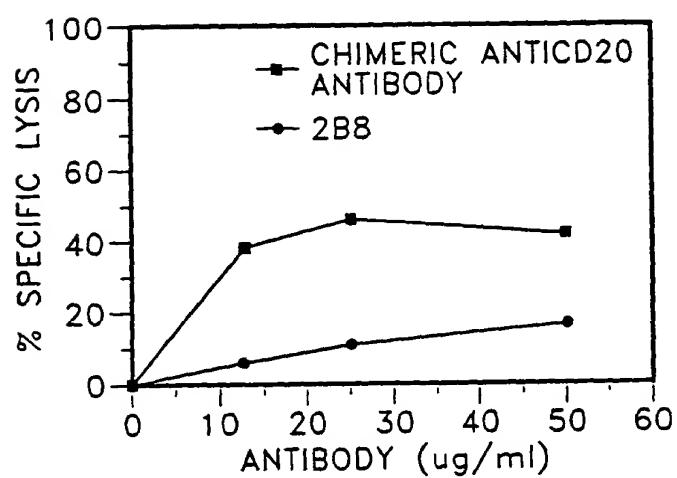


FIG. 7

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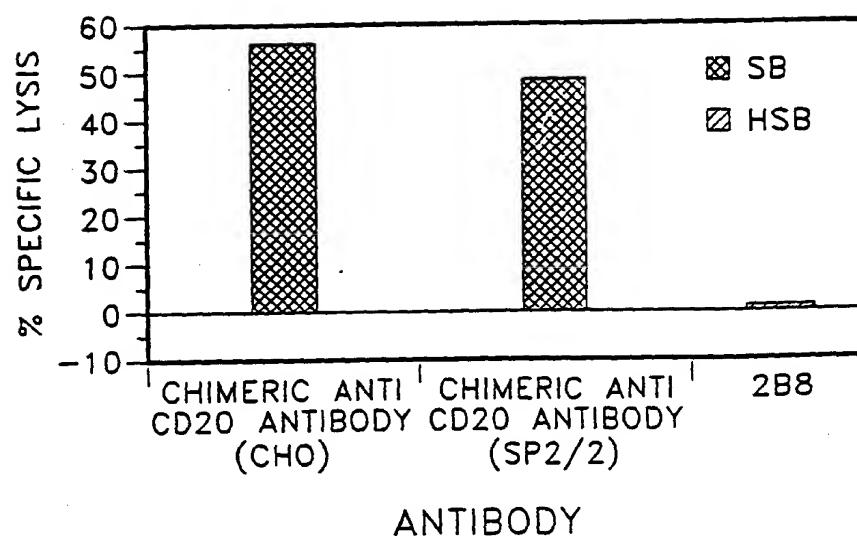


FIG. 8

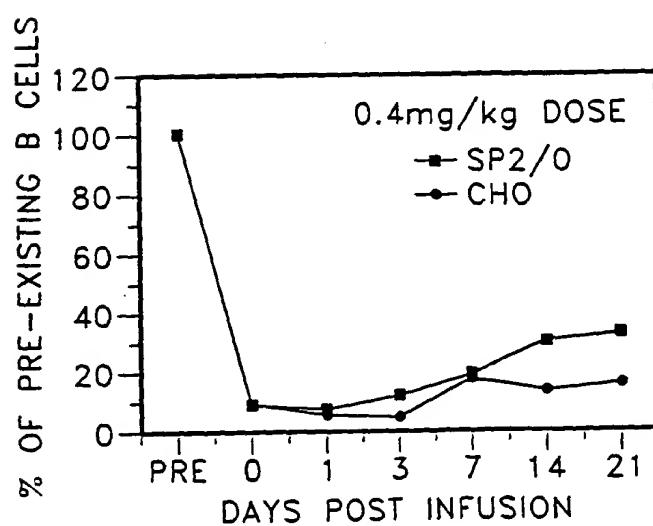


FIG. 9A

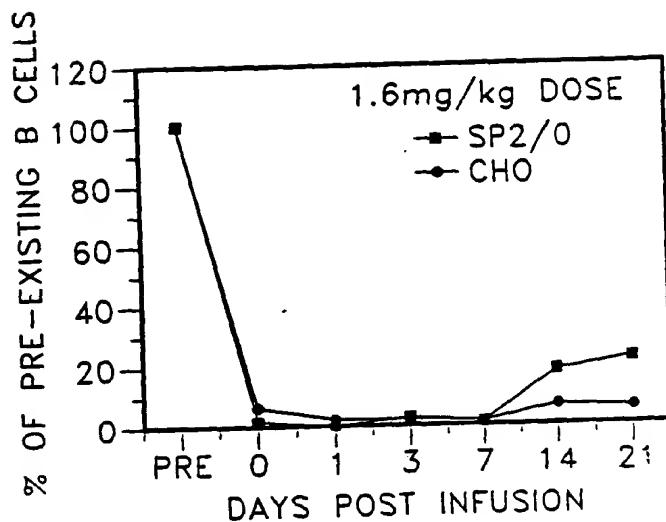


FIG. 9B

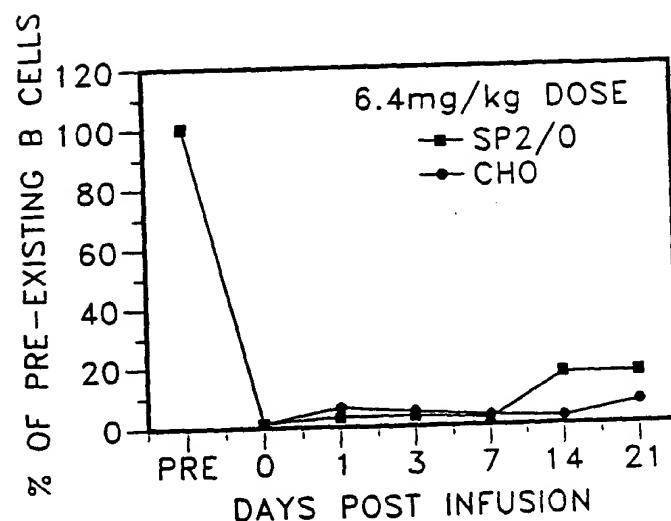


FIG. 9C

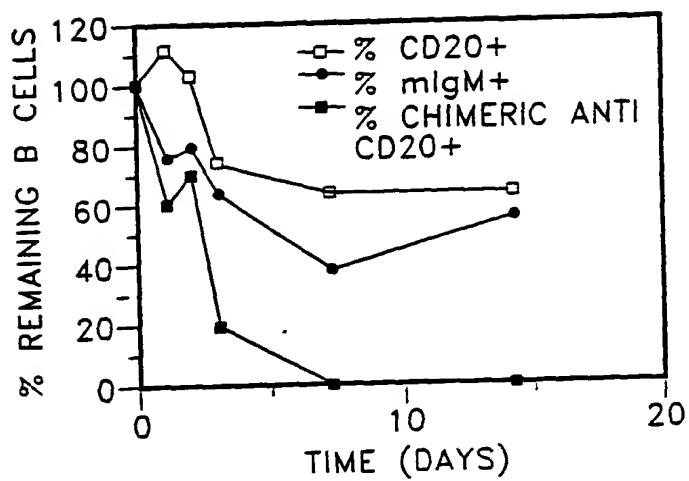


FIG. 10

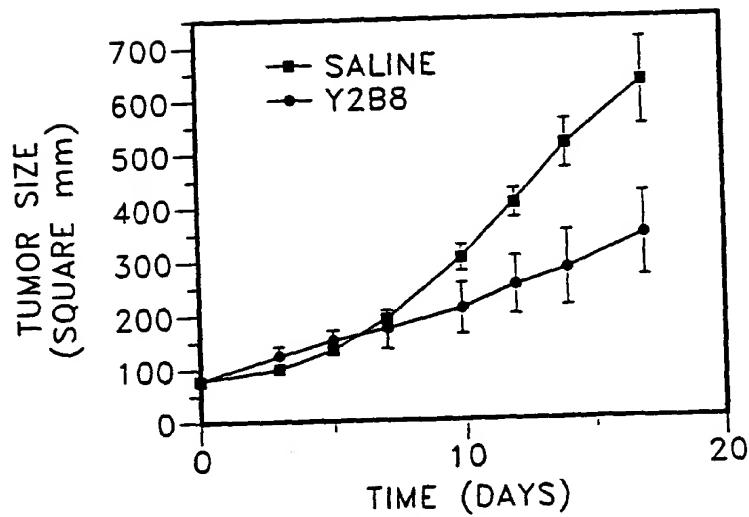


FIG. 11

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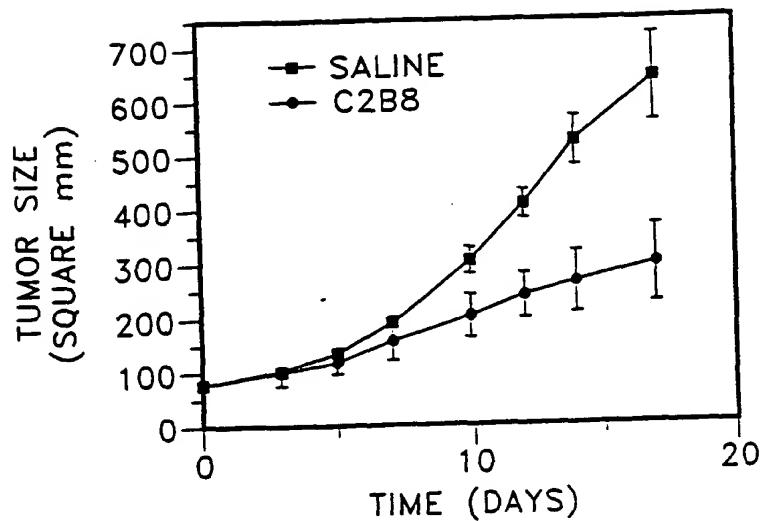


FIG. 12

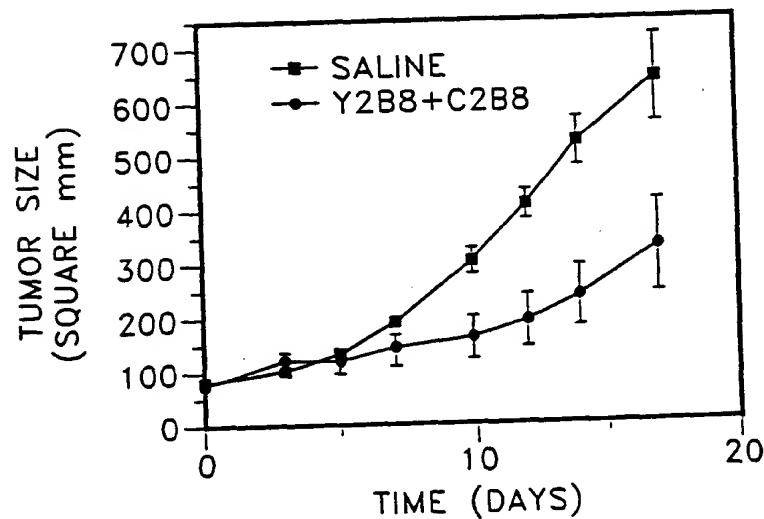


FIG. 13

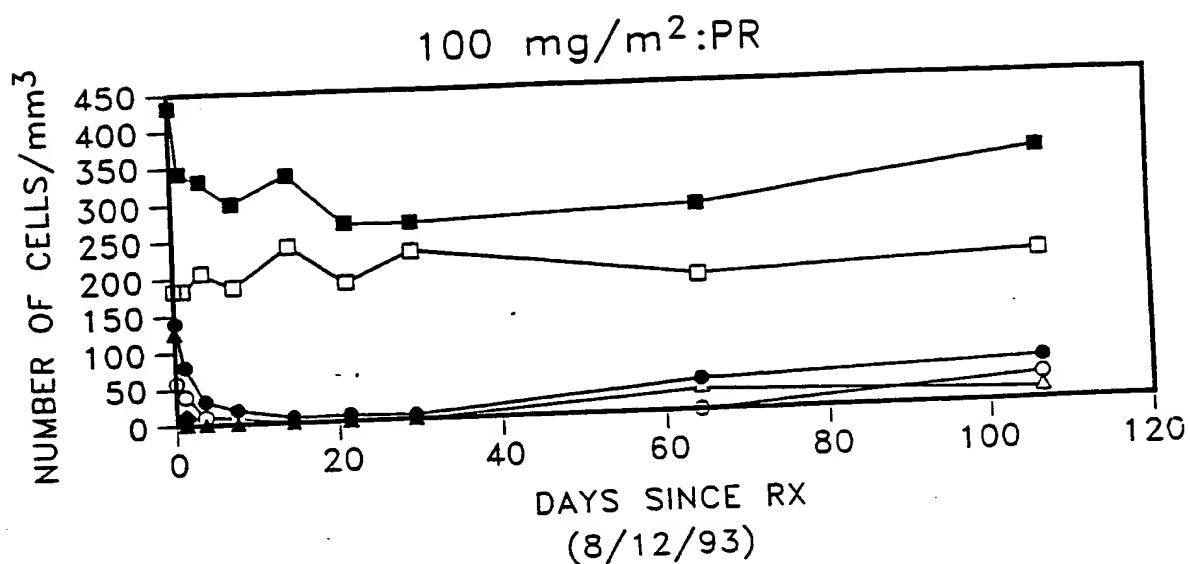


FIG. 14A

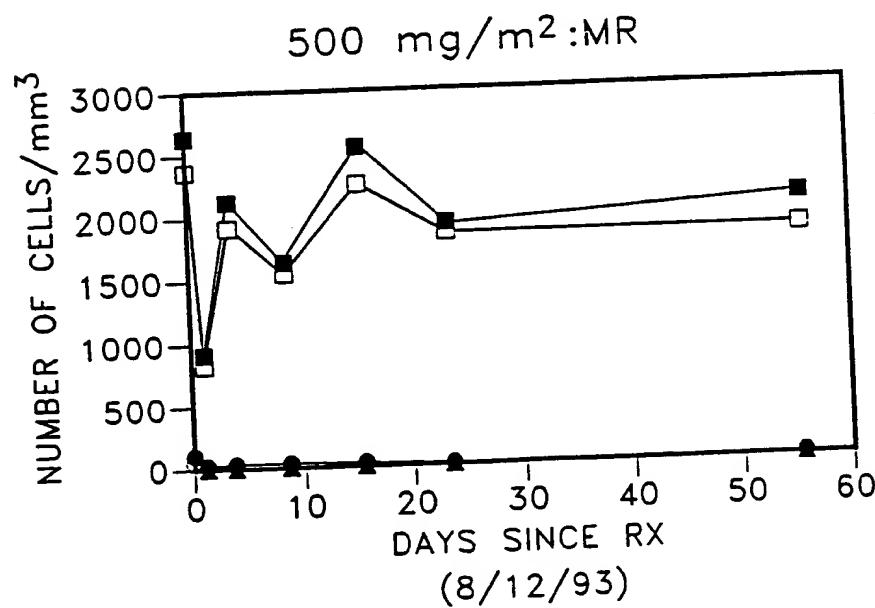


FIG. 14B